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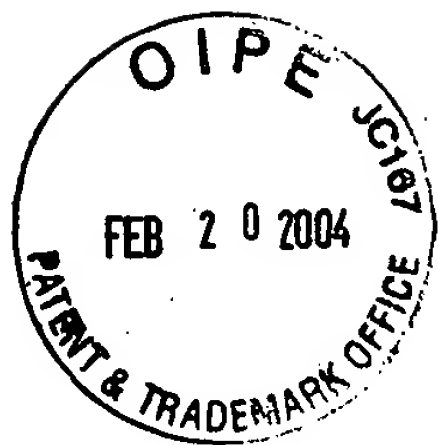
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Replacement Sheet

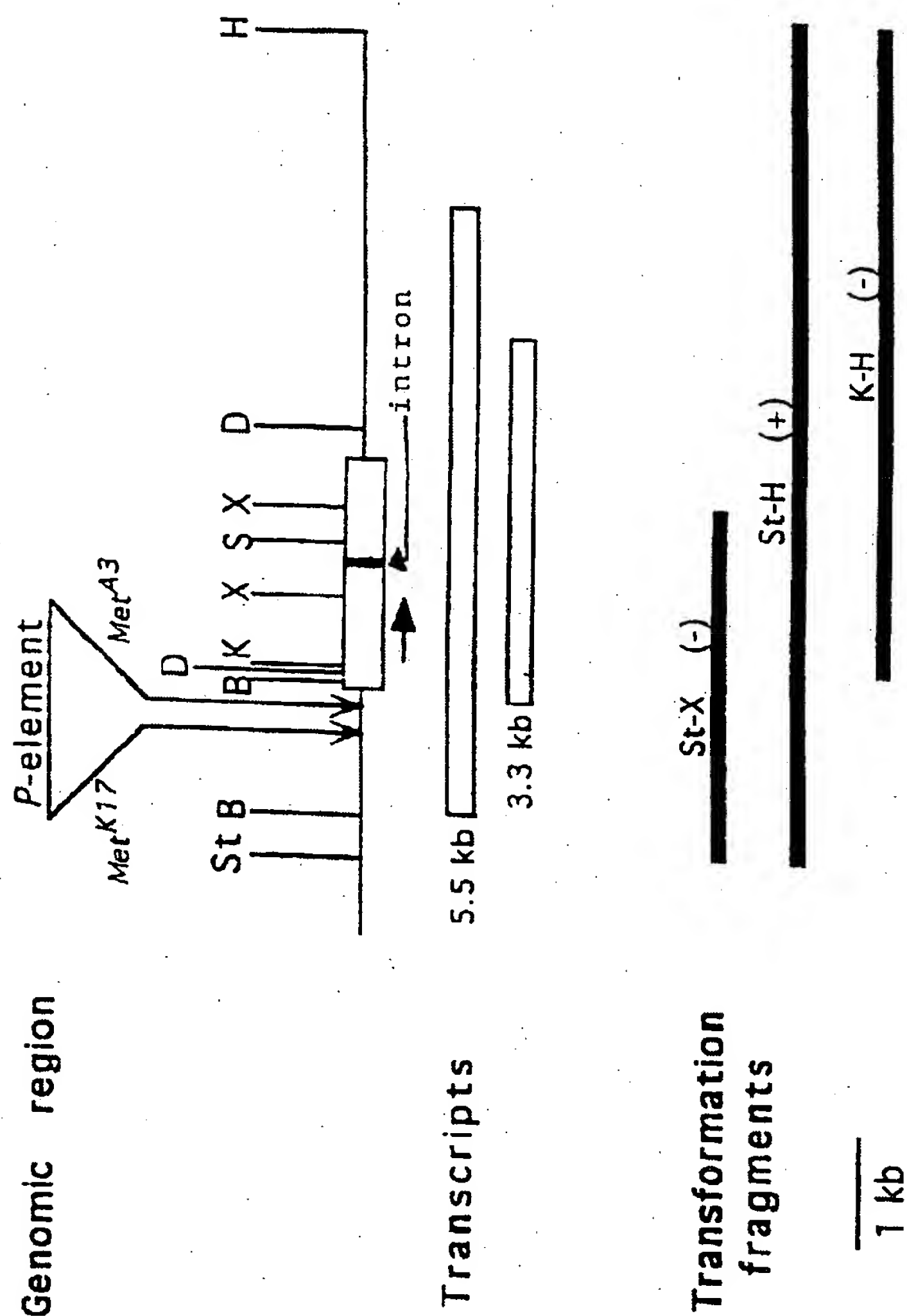


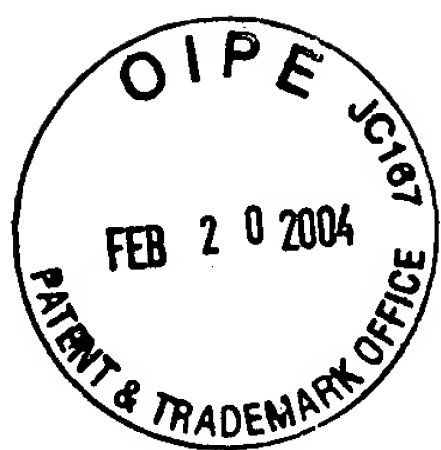
FIGURE 1

Replacement Sheet

6.2341b GENOMIC

AGGCGCTGACATTTGTAATCAGGTGGCTCAATCATTATAGCCATCCTTATCGAAGTCGATGTTCTCGCGGCCAACTCGATGACCTGCAAAATGAATAGT
101 GGGCAAAATGTTTGGGATCATTGAAATAAATGACTCCATGATTGAGTGCACCCACCTCTTGGCCCTGAAAGTGTCCGCAACCATGGGGCACTCCCAATGA
201 ACTCGAACCGACCCCTTTCGGGGGGGGCCAGCTCACCOCGAGATTGATCTTTAGCTTTGTGGTTGTCTGTGGACTTGGCCAGCAAAAGTGGATCCCGCAAG
301 CTCTCCAGCGGAAACCATATGCTCAGCGTTTGGCCCGGAAAACTGCTTCAGCATGCCCCCGTTGATATCGAGCGTGGATCAAAAGCATCATATAAATCTC
401 CTCAGTTTAAATACTTCAMAAACGCAATTTTCAGCAGAAATGAAATCCGTTAAACAAGAAAGAGCGCCAACTAGTTATCGAGCGTCTTAATCGATAAT
501 AAAATTCATGACGTCTGCTATCGAAATATTTCGAATTTTGTAGCAAAATTTTATGGGATTATTGTACATCAAAAGTTATTACATTATTACTGTGG
601 ACTTATGTTATTATAAAGAAATTAATAAAATAATTTATAATAGAAATATAAAAGAGCTGTAGATTACATGTATTACAACAATGTTATCGACAGCGAA
701 CAAGATGTTTCGATCTTTCTGATATTTTGTCCGGTGTGAACGTGCGAATTTTAGTAGCACAACCGATTACATCGATTATTCGATAGTTTATAGACTGGCC
801 AAGTTTATTTTATATAATAA
901 CGCCCTCCGAATTTCCCTTATTCGGGGCTTAATAATCGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA
1001 ATCAAAACGTAAAAAAGGAAAAAATAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
1101 GGAAGATGACGAAAGCGAAAGAGGAAACATATGTACTTGGGTGAGAGTGACGT
1201 GAGGCGAGCAAAACCAAAACCAACAGCAGCACAGCATAAGCGAGAGCTTGAATACTTTAAAGCGCAAAAAAACAAGACAAACAGCCCAAAATAA
1301 GAACTAAAACTGCCAAAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
1401 TGACATTTTTCATTTCACCGAAGCGCCCAATTAAGGCGAAATTCATAAATOGAGGATTACAGGTGGAAGAACAGGAGGCACTATCCGAGAAACCGCC
1501 CAAAAAGTCCAAATGCGACACACAGAGACCGGCAACACCGGCTCCACAGGATCCGCTGGCTCGACAGGATCCGGATCCGGATCCGGATCCGGATCCGG
1601 AGCTCTCAGATCCGACGAATGACGCGGAGCGCCCTTAACCTTGGCGAAACACAGCGAGCGGATAGCTTAATGCCAGCATCCAGGAGCTGGCCACCATG
1701 TACCACATCGACCGAATCTCCGCTCGCTGGACAAACCCGCGCTCTAGATTTCGCGACCCATTCGCTTGCAGCTTCAGTATGCTTTTGGCAAGTCCGC
1801 TTCAGAGCTGCCAAGAAACCGGCTCAAGGACAGCGGTATGCTTCCCTCACTTCTCGAGATCTAACCAATCCAGTCTGCATTAACCGGACACTCTA
1901 ATGCAACTCTCGACT
2001 ATTTGTATGCGCAGAACTCTACTCGAGATCAAGCTATCCGATGATCAGGATCTGTTAAGACAGCAGCTAATACCCAGGATATAGAGACCTGTTCTATCA
2101 GCATCAGCCACCCACGACGAGCGAGCCACAAATCCCGAG
2201 ACGGAGAACACCTCTGGGTCCGAGCAGGAG
2301 TGGGACCATTTGATGACCGACTACGCATGATGCGCGCTGCTTTACGTTCCGCTTGGCTAGGCTTCCACGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAG
2401 GOTTAGATCGATGGCTGCTTTCTGTCGAGTGACTCTCTCTTAACCGGAGGTGCGCGCTGCCAACTTCCGATTTGCTTCCGATTTGCTTCCGATTTGCT
2501 AACAACAATATCTGCTGCTGCTGCTGCGAGCAGTGCGCAGAGAAAGCGGAGCGGTGCCACCCAGCAGATGCCATTGCCAGCGCGGCTGATACGAGCTGAGA
2601 GCGCAATGATATGTTCTGCTGCTGCTGCTGCGAG
2701 GCGAAGCCCTATCACTGAGTAACTATCGAGGACCTTAATCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
2801 GATGAGGTGGTATATTAACTATCT
2901 CATGCACTGGAGCAGCTTCCGCTGGGTGATTGTGGCCCTTCGACAAATGTACGATTGCAACAGTGACTATGGCGAGGAGCTCTCACTCTCTCTCTCTCT
3001 CAAAGCGGCTTCATTTAACCTGCAACCAAGGATTTCTGAGAGGTGACCGGTGCCAGTAAATAGGTGCATTTCTTCTGTGCTCAACAGCTCTCTCTCT
3101 GAGGAGGCGGGCGGGCAAAAGGTGCGAGGAGTGAAGAGGAAATTCGCAAACTCATAGGCGGAGATGCCACGCGAGCAGCAGCTCCGATTTGCGCG
3201 CCTCCAGGCAACCGCAGCACTTGAGAGATTTGCT
3301 GCAAGGCTTAATGAGAGTGGCTACAGTTGCCAGCAAAATCCTTAACCTCTCGAGGAGTTAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
3401 CTTCCCTCATCGGTCAAGAGCTCCATCTCCAAGTCTGTTGAGTGTGTTCAATGTGACCGCGGCGCAAAAGTTTCAGCAGGAGCATCAGAGGACCGGTGAAC
3501 GTGACCTGACAGCTTAAGAGCGGCAACCATCCAGCGAGGCGGTATCGCGCACTGAGCAGCTGCCATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
3601 ATCACCAGCCAGTAGCTTGAAGTGCAGCGAGGAGCAGCAGCAGCGGCTCCGACCAACCATCCGCGCAAGCTGCTTACAGCAGGAGCGGTTGCGCGGAGGAGGAG
3701 CTGCATCGAAGCTGACAGCAGCGCTCGGATGACGCGGCTGATGGAACCTGGTTTGGCTCTCAATTTGGGTGTGTGAAATGGAAGTAAATGAGTCTCAG
3801 TCCGCAAAACGAATTAGTATCGGTAAATTAATCTCGGCAATCGCAATGTGAAAAACCAAAATGTATCAGAAAAAAGAGGAGGAGGAGGAGGAGGAGGAGGAG
3901 AAAATTCAGCAGAAAACTTAAATACGAAAAAAGAGCGGTGGGTGAAGAACCTTTTGTTTTCAATTTCCAGCTTTTGGCAATCAAAACAA
4001 TTTTAATTTTCAGTATACATATGTATATAAGTTAGTTGCTTTTACAAAGCTATTAACAAATCAAGCAATTTGTAAATTTAATATGAGACTTTCCGTTGATT
4101 TTTGCTTTCTACGTAATTTTCGACTTCAATTGATCTATAGGTTTCCGATTAATAAAGCAAAATTAACGTTTTCATTTTGATGAAAATGCAATATGAGT
4201 CGCATTTATTTGATATATGACAGTAATATATGATCTGATCAGGATTAATGTTTCTCAAAACATTAAGGATACATTTTGGTGTGACTTTGCCATTACTG
4301 TTTCTGTGTGATTTTCGGTATAAATAGTAGTTTGAATACATGTTATATTGATGAATGGGATCGGTGGGTGCTGCTAAATCGCTTCCATTATCAATAA
4401 TTTCTGTGTGATTTTAACTTAACTTTTAAATGATATGATGCGAGCGTGAAGTGAATTTGTGATGCTGTGAGCTGGGTGTGAATGAACATTAGATCA
4501 GTGCTCGGATTTGGTTTAACTTGAATTTAAACCCATTTCCGAGTTTCCGATTTACCTTCCGCGCCCAACCACTTGTAAAGAGATCAAAAA
4601 AAAAAAAGAAAGAAATAGAAAAAACAACAAACAAATATATTTTATTTCCGCTTAAGCTTGAAGCTGTAACCACTTATTAAGTTAAACAAAC
4701 GGAATGTTCAATCGATGAAATTAACCGCTGCTTTTGAATTTTGGCGTCTCGCTCGAAGAAAGAAAGAGGAGTACTACATATGATCAGTCAAACTAATCC
4801 AAGTCAAACTCTCACTGCTCAGAAATGGAGACTTTATTAAGGTTTATTTATTTATGAAGAAATAGCATATATTTTATATATATATTTATGATATAT
4901 TATTTATATCAAAATCTCTCTCGATATCTCTTGTATCTATAAAACCTTCCAGGCGAGCTTTATTTTCAACAGTTTAAATTTTGGGAACTTTAC
5001 AAAGCATATAGCATACCCCAATCCATATCTTTAAATCTTTGTAGTTATTTACAAATGTGTCAAAATTAATAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
5101 AATCGCTAAATACAAATATATCAATTTAAATGATCTATGTTACCTTCTATAATGCTCTACTGGACAAATATGATTAAGTTGAATTTCAAAATGTTT
5201 TGAAGTTTGTACTAAGGAGTTTGGCTGTAGTTCAATACTACAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
5301 ATTGCTTGGCGTTGGCTTCTATACCGCGGTATGGAAGGAG
5401 GGTTCGCGGGGTTTGGGGGAACCGCGTTGGTGTATGGGCGAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
5501 TCTCTAGCTATAAATGATATGATATATATGCTATTAATTTTGGTTAGCTCAATTTTGTGTGATTTTGTATATATATATATATATATATATATATATAT
5601 GTAAATAAATAAATCCCAATCTAATTTCCCGAGGAGTCTTCAGTGTGTTTCAACAGGTTGTGCTCTTTAAACACTTTTGGCTTATCTCTTTCATT
5701 TAAATTTTGTGTGTTTCT
5801 GTGAGAGGATATCTCTGTATAGAAATTAATGTGTATATTTGAAAGTTTGAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT
5901 TAATTAATATACCAATTAACAGTTTCAATGAAACCTTAATAAATAAATAATATATAAAGAGAGTGAAGTGTGTTTCAATCAATGAAAGTTACTTC
6001 CTATTTCTAGGAGTTGGAATGTACACTTTTATTAAGCTGATTTGAAATGCGGCCACATATATCTGCTTGGCGCAAGCATTCGACGCGATTAACG
6101 CGCAATTAACCTCCCGCAGAGGTGAGTTTGAACATGCAATTAATCGATTGCCATTCGGAACCAAAAAACACCTTGAGTTTGGTCAGATCGGTTTGGCG
6201 GGGATAAATAAATAAATTAATTAATTTTCTTTT

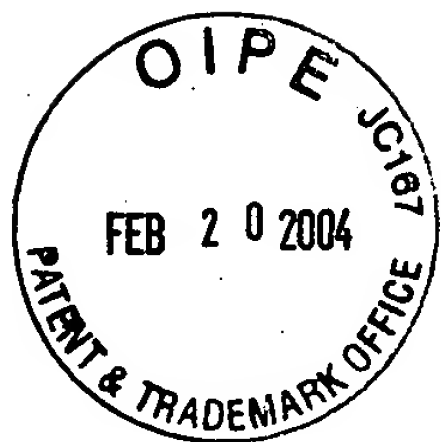
FIGURE 2



Replacement Sheet

1	10	20	30	40	50	60	70	80	
1	10	20	30	40	50	60	70	80	Notion
1	10	20	30	40	50	60	70	80	cDm
81	90	100	110	120	130	140	150	160	Notion
77	90	100	110	120	130	140	150	160	cDm
161	170	180	190	200	210	220	230	240	Notion
157	170	180	190	200	210	220	230	240	cDm
241	250	260	270	280	290	300	310	320	Notion
237	250	260	270	280	290	300	310	320	cDm
321	330	340	350	360	370	380	390	400	Notion
317	330	340	350	360	370	380	390	400	cDm
401	410	420	430	440	450	460	470	480	Notion
397	410	420	430	440	450	460	470	480	cDm
481	490	500	510	520	530	540	550	560	Notion
477	490	500	510	520	530	540	550	560	cDm
561	570	580	590	600	610	620	630	640	Notion
557	570	580	590	600	610	620	630	640	cDm
641	650	660	670	680	690	700	710	720	Notion
637	650	660	670	680	690	700	710	720	cDm
721	730	740	750	760	770	780	790	800	Notion
717	730	740	750	760	770	780	790	800	cDm
801	810	820	830	840	850	860	870	880	Notion
797	810	820	830	840	850	860	870	880	cDm
881	890	900	910	920	930	940	950	960	Notion
877	890	900	910	920	930	940	950	960	cDm
961	970	980	990	1000	1010	1020	1030	1040	Notion
957	970	980	990	1000	1010	1020	1030	1040	cDm
1041	1050	1060	1070	1080	1090	1100	1110	1120	Notion
1037	1050	1060	1070	1080	1090	1100	1110	1120	cDm
1121	1130	1140	1150	1160	1170	1180	1190	1200	Notion
1117	1130	1140	1150	1160	1170	1180	1190	1200	cDm
1201	1210	1220	1230	1240	1250	1260	1270	1280	Notion
1197	1210	1220	1230	1240	1250	1260	1270	1280	cDm
1281	1290	1300	1310	1320	1330	1340	1350	1360	Notion
1277	1290	1300	1310	1320	1330	1340	1350	1360	cDm
1361	1370	1380	1390	1400	1410	1420	1430	1440	Notion
1357	1370	1380	1390	1400	1410	1420	1430	1440	cDm
1441	1450	1460	1470	1480	1490	1500	1510	1520	Notion
1437	1450	1460	1470	1480	1490	1500	1510	1520	cDm
1521	1530	1540	1550	1560	1570	1580	1590	1600	Notion
1516	1530	1540	1550	1560	1570	1580	1590	1600	cDm
1601	1610	1620	1630	1640	1650	1660	1670	1680	Notion
1528	1610	1620	1630	1640	1650	1660	1670	1680	cDm
1681	1690	1700	1710	1720	1730	1740	1750	1760	Notion
1688	1690	1700	1710	1720	1730	1740	1750	1760	cDm
1761	1770	1780	1790	1800	1810	1820	1830	1840	Notion
1688	1770	1780	1790	1800	1810	1820	1830	1840	cDm

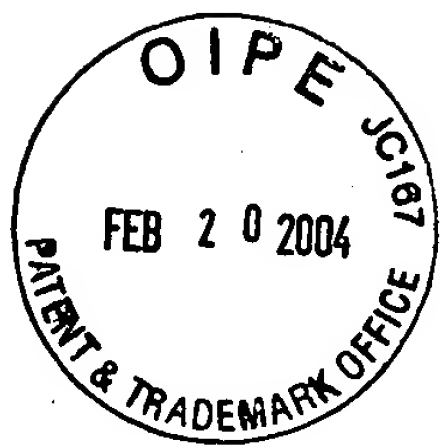
FIGURE 3A



Replacement Sheet

1841	ATGAAGGAGAAATTCCTGACAAATCATCAAGGCGGAGATGCCACGAGAGGAGCAGTCCGATTTCGGCGGCTCGAGGC	MetGen
1842	ATGAAGGAGAAATTCCTGACAAATCATCAAGGCGGAGATGCCACGAGAGGAGCAGTCCGATTTCGGCGGCTCGAGGC	cDNA
1921	ACCGCAGCAACTTGAGAGAAATGTTCTCTATCTAATAGAGAACTACAGAAAGAGTGTGGATTACAGCAGACCGTTGGCG	MetGen
1922	ACCGCAGCAACTTGAGAGAAATGTTCTCTATCTAATAGAGAACTACAGAAAGAGTGTGGATTACAGCAGACCGTTGGCG	cDNA
2001	CCGAGGCAATGGAAGCCCTAAATGGACGATGGCTACAGTTCGCGAGCAAAATACCTTAACCTCTCGAGGAGTTAGCTCCCTCG	MetGen
2002	CCGAGGCAATGGAAGCCCTAAATGGACGATGGCTACAGTTCGCGAGCAAAATACCTTAACCTCTCGAGGAGTTAGCTCCCTCG	cDNA
2081	CCGAGGCAATGGAAGCCCTAAATGGACGATGGCTACAGTTCGCGAGCAAAATACCTTAACCTCTCGAGGAGTTAGCTCCCTCG	MetGen
2082	CCGAGGCAATGGAAGCCCTAAATGGACGATGGCTACAGTTCGCGAGCAAAATACCTTAACCTCTCGAGGAGTTAGCTCCCTCG	cDNA
2161	CCGAGGCAATGGAAGCCCTAAATGGACGATGGCTACAGTTCGCGAGCAAAATACCTTAACCTCTCGAGGAGTTAGCTCCCTCG	MetGen
2162	CCGAGGCAATGGAAGCCCTAAATGGACGATGGCTACAGTTCGCGAGCAAAATACCTTAACCTCTCGAGGAGTTAGCTCCCTCG	cDNA
2241	TGTGACGCGCGCCAGAAAGTTTCAGCAGGAGGATCAGAAAGAGGCTGAACCTGACCGTGAAGGAGCTTAAGGAGCGCA	MetGen
2242	TGTGACGCGCGCCAGAAAGTTTCAGCAGGAGGATCAGAAAGAGGCTGAACCTGACCGTGAAGGAGCTTAAGGAGCGCA	cDNA
2321	ACTCCAGCAGGCGCTGATCCGCAACTGAGCAGCTGCTTAAGCGAGGCGGAAACGCTATCTATCTATCAACAGCC	MetGen
2322	ACTCCAGCAGGCGCTGATCCGCAACTGAGCAGCTGCTTAAGCGAGGCGGAAACGCTATCTATCTATCAACAGCC	cDNA
2401	AGTAGCTTGAGTCCAGCGAAGCAACCGGACAGCGGCTGCTTAAGCGAGGCGGAAACGCTATCTATCTATCAACAGCC	MetGen
2402	AGTAGCTTGAGTCCAGCGAAGCAACCGGACAGCGGCTGCTTAAGCGAGGCGGAAACGCTATCTATCTATCAACAGCC	cDNA
2481	TCCCAATGCTCTGATCGAAGCCCTGACCAAGCAAGCTGCGATGAGCGGCTGATGGAACCTGGTTTCCCTTCTAATTTGGTG	MetGen
2482	TCCCAATGCTCTGATCGAAGCCCTGACCAAGCAAGCTGCGATGAGCGGCTGATGGAACCTGGTTTCCCTTCTAATTTGGTG	cDNA
2561	TGTGAAATGGAGCTAATTTGGTACCTCAGCTGCGGACAAACGAAATAGTATCGGTAATATAATCTTGGCAATCGCAATG	MetGen
2562	TGTGAAATGGAGCTAATTTGGTACCTCAGCTGCGGACAAACGAAATAGTATCGGTAATATAATCTTGGCAATCGCAATG	cDNA
2641	TGAAAAACCAAAATGTATCAGAAAAAAACGAGCATTATTCAAAATAGTTTAAAAATTCAGCCAAAAAATTAATAACGAA	MetGen
2642	TGAAAAACCAAAATGTATCAGAAAAAAACGAGCATTATTCAAAATAGTTTAAAAATTCAGCCAAAAAATTAATAACGAA	cDNA
2721	AAAAAAGAGCGTGGGTTGAAGAACCTTTTGTTCATATTACATTTCCAGCTTTGAGCAATCAAACTTTTAAATTTT	MetGen
2722	AAAAAAGAGCGTGGGTTGAAGAACCTTTTGTTCATATTACATTTCCAGCTTTGAGCAATCAAACTTTTAAATTTT	cDNA
2801	CAGTATACATATGTATAATGAGTTGCTTTACAAAACTTATTAACAAATCAAGCAATTTGTAATTTAATATGAGACT	MetGen
2802	CAGTATACATATGTATAATGAGTTGCTTTACAAAACTTATTAACAAATCAAGCAATTTGTAATTTAATATGAGACT	cDNA
2881	TTCCGTCATTTTGGCTTTTACCTTCTTTCGACTTCAATTTGATCTATAGGCTTTCCGATTAATAAACGAAATTAACGCT	MetGen
2882	TTCCGTCATTTTGGCTTTTACCTTCTTTCGACTTCAATTTGATCTATAGGCTTTCCGATTAATAAACGAAATTAACGCT	cDNA
2961	GTTCATTGATGAAATGCAATATGAGCTCCGATTTATTTGATATTATGACAGTAATAATGATCTGATCAGCAATATC	MetGen
2962	GTTCATTGATGAAATGCAATATGAGCTCCGATTTATTTGATATTATGACAGTAATAATGATCTGATCAGCAATATC	cDNA
3041	GTTCATTGATGAAATGCAATATGAGCTCCGATTTATTTGATATTATGACAGTAATAATGATCTGATCAGCAATATC	MetGen
3042	GTTCATTGATGAAATGCAATATGAGCTCCGATTTATTTGATATTATGACAGTAATAATGATCTGATCAGCAATATC	cDNA
3121	CATTAGATCACTGCTCGGATTTGGTTTATGTTGAAATTTAAACCCCATTTCCCGCATTTTCCAGTTATCACCTTCCGCT	MetGen
3122	CATTAGATCACTGCTCGGATTTGGTTTATGTTGAAATTTAAACCCCATTTCCCGCATTTTCCAGTTATCACCTTCCGCT	cDNA
3201	CAAAACACCATTTGTAATAAGAGTACAAAAAAGAAAGAAATAGAAAAACAAAAA	MetGen
3202	CAAAACACCATTTGTAATAAGAGTACAAAAAAGAAAGAAATAGAAAAACAAAAA	cDNA

FIGURE 3B



Replacement Sheet

1 MAAPETGNTGSTGSAGSTGSGSGSGSGSGSSSDPANGREA AA Genomic
1 MAAPETGNTGSTGSAGSTGSGSGSGSGSGSSSDPANGREA cDNA

41 RNLAEKQRRDKLNASIQELATMVPHAAESSRRLDKTAVLR AA Genomic
41 RNLAEKQRRDKLNASIQELATMVPHAAESSRRLDKTAVLR cDNA

81 FATHGLRLQYVFGKSASRRRKKTGLKGTGMSASPVGDLPN AA Genomic
81 FATHGLRLQYVFGKSASRRRKKTGLKGTGMSASPVGDLPN cDNA

121 PSLHLTDTLMQLLDCCFLTTLTCSGQIVLVSTSV EQLLGHC AA Genomic
121 PSLHLTDTLMQLLDCCFLTTLTCSGQIVLVSTSV EQLLGHC cDNA

161 QSDLYGQNLLQITHPDDQDLLRQQLIPRDIETLFYQH QHH AA Genomic
161 QSDLYGQNLLQITHPDDQDLLRQQLIPRDIETLFYQH QHH cDNA

201 QQQGHNPPQQHSTSTSSASXSGSDLEEEEMETEEHRLGRQQG AA Genomic
201 QQQGHNPPQQHSTSTSSASA SGSDLEEEEMETEEHRLGRQQG cDNA

241 EADDDDEDHPYNRRTPSPRRMAHLATIDDRLRMDRRCFTVR AA Genomic
241 EADDDDEDHPYNRRTPSPRRMAHLATIDDRLRMDRRCFTVR cDNA

281 LARASTRAEATRHYERVKIDGCFRRSDSSLTGGAAANYPI AA Genomic
281 LARASTRAEATRHYERVKIDGCFRRSDSSLTGGAAANYPI cDNA

321 VSQLIIRRSRNNNMLAAAAAVAAEAATVPPQHDAIAQAALH AA Genomic
321 VSQLIIRRSRNNNMLAAAAAVAAEAATVPPQHDAIAQAALH cDNA

361 GISGNDIVLVAMARVLREERPPEETEGTVGLTIYRQPEPY AA Genomic
361 GISGNDIVLVAMARVLREERPPEETEGTVGLTIYRQPEPY cDNA

401 QLEYHTRHLIDGSIIDCDQRIGLVAGYMKDEVGILTSSL AA Genomic
401 QLEYHTRHLIDGSIIDCDQRIGLVAGYMKDEVGILTSSL cDNA

441 TAYDN SCTLH SKQVRNLSPF CFMHLDDVRWVIV ALRQMY AA Genomic
433 RNLSPFCFMHLDDVRWVIV ALRQMY cDNA

481 DCNSDYGESCYRLLSRNGRFIYLHTKGFLEVDRGSNKVHS AA Genomic
458 DCNSDYGESCYRLLSRNGRFIYLHTKGFLEVDRGSNKVHS cDNA

521 FLCVNTLLDEEAGRQKVQENKEKFSTIIKAEMPTQSSSPD AA Genomic
498 FLCVNTLLDEEAGRQKVQENKEKFSTIIKAEMPTQSSSPD cDNA

561 LPASQAPQQLERIVLYLIENLQKSVDSAETVGGQGME SLM AA Genomic
538 LPASQAPQQLERIVLYLIENLQKSVDSAETVGGQGME SLM cDNA

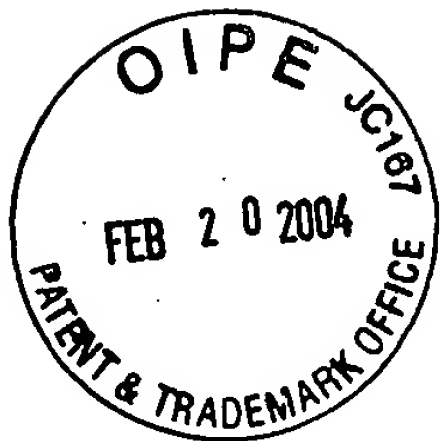
601 DDGYSSPANTLTLEELAPSPTPALALVPPAPSSSVKSSISK AA Genomic
578 DDGYSSPANTLTLEELAPSPTPALALVPPAPSSSVKSSISK cDNA

641 SVSVVNVTAARKFQQEHQKQRERDREQLKERTNSTQG VIR AA Genomic
618 SVSVVNVTAARKFQQEHQKQRERDREQLKERTNSTQG VIR cDNA

681 QLSSCLSEAETASCI LSPASSLSASEAPDTPDPHSNTSPP AA Genomic
658 QLSSCLSEAETASCI LSPASSLSASEAPDTPDPHSNTSPP cDNA

721 PSLHTRPSVLHRTL TSTLR AA Genomic
698 PSLHTRPSVLHRTL TSTLR cDNA

FIGURE 4

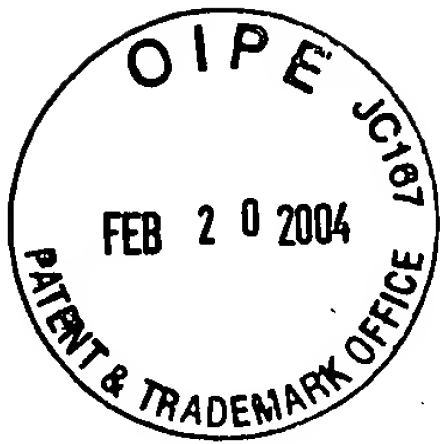


Replacement Sheet

1 ATGGCAGCACCGGCAACACGGGCTCCACAGGATCCGCTGGCTCGACAGGATCGGGATCGGGATCGGGAAGTGGAGC A
1 CAGCAGACGGGCAACACGGGCACACAGGATCAGCTGGGTCCACA-----GGATCGGGATCGGGAAGTGGAGC B
91 TCCTCAGATCCAGCGAATGGACGGGAGGCCCGTAACCTTGCCGAAAAACAGCGACGGGATAAGCTTAATGCCAGCATCCAGGAGCT A
72 TCCGCAGATCCAGCGAATGGACGGGAGGCCCGCAATCTTGCCGAGAAACAGCGACGGGATAAGCTTAATGCCAGCATCCAGGAGCT B
181 GGCTACCATGGTACCACATG-CAGCCGAATCCTCCCGTCGCCCTGGACAAAACCGCCGTCCTTAGATTGCCACCC A
158 GGCTACCATGGTACCACATGTCAGCCGAATCCTCCCGACGCCCTGGACAAAACCGCCGTCCTCAGATTGCCACCC B

FIGURE 5

Replacement Sheet



Replacement Sheet

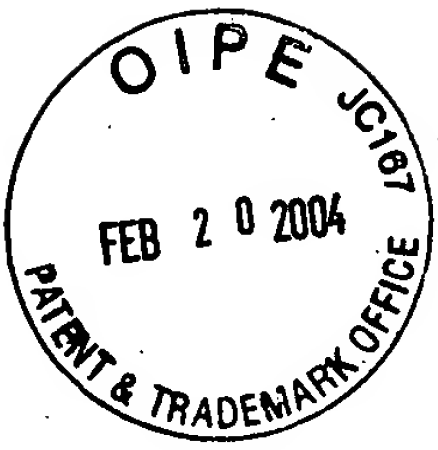
Fig. 6C

..... M D E A N I Q D K
K F L R C D D D Q M S N D K E R F A R S D D E Q S S A D K
D Y Q E S M D T D K D D P H G R L E Y T E H Q G R I K N .
..... M N S S S A N I T Y A S R K R R K P V Q K T V
..... L L ..
..... E L K H L I L . E A A D G . F L F V
..... E L K H L I L . E A A D G . F L F I
..... E L K H L I L . R A A D G . F L F V
S P V G D L P N P S L H L T D T . L M Q L L D C C F L . T
R A A N F R E G L N L Q E G E F L L . Q A L N G F V L . V
.....
N A G R I L D L K S G . T V K K E G
L T G R I L D L K T G . T V K K E G
P R E R L I D A K T G L P V K T D I
S G S D L E E E E M E T E E H R L G R Q Q G E A D D D E D
E A T G L P Q T V V C Y N P D Q I P P E N S P L M E . . .
.....
W P P T D M F P N M H M E R D V D
W P P A G V . . S L P D D D P E A
W P P T K M . . G L D E D N E P D
R N N N M L A A A A A V A A E A A T V P P Q H D A I A Q A
..... L H G Q K K K G K D G S I L P P Q
..... H . . D
C Y D F F H P E D Q S H M K E S F D Q V L K Q K G Q M F S
I V E F C H P E D Q Q L L R D S F Q Q V V K L K G Q V L S
C Y E Y F H Q D D I G H L A E C H R Q V L Q T R E K I T T
P F C F N H L D D V N W V I V A L R Q M Y O C N S D Y G E
G Y Q F I H A A D M L Y C A E S H I R M I K T . G E S G M
.....

Match Line to Fig. 6B

Match Line to Fig. 6D

Match Line to Fig. 6G



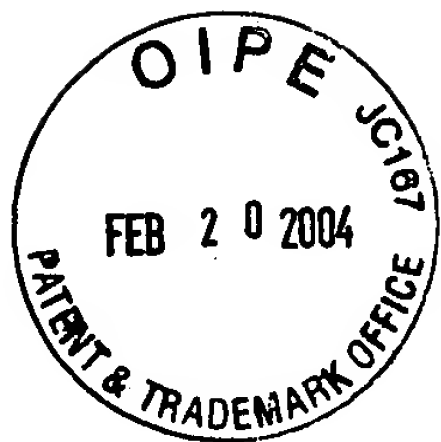
Replacement Sheet

Fig. 6D

.....	Consensus
ERFASRENHCEIERRRRNKMTAYI	Darnt
ERLA-RENHSEIERRRRNKMTAYI	Harnt
- - - AREAHSQIEKR RRD KMNSFI	Bmal1
- - - - REARNLAEKQR RDKLNASI	Met_Orf
KPIPA-EGIKSNPSKRHRDRLNTE	Ahr_Human
PAS A	
..... S . S L . . . Q	Consensus #1
VSCDSGRVIYVSDSVTPV-LNYTQ	Darnt
VSCETGRVVYVSDSVTPV-LNQPQ	Harnt
VGCDRGKILFVSESVFKI-LNYSQ	Bmal1
LTC-SGQIVLVSTSV EQ L-LGHCQ	Met_Orf
VITD-ALVFYAS-STIQDYLG FQQ	Ahr_Human
.....	Consensus #1
H QSSMR L SMGA	Darnt
Q QSSMR M CMGS	Harnt
T PGPSRLCSGA	Bmal1
HPYNRRTPSPRRMAHLATIDDR LR	Met_Orf
.....	Ahr_Human
..... L . A L	Consensus #1
. . . DMSSH-CCLVAIG-R-LQVTS	Darnt
. . . GQGSK-FCLVAIG-R-LQVTS	Harnt
. . . NEGCLNSCLVAIG-R-LHSHV	Bmal1
ALHGISGNDIVLVAMA-RV L REER	Met_Orf
..... LALFMIA TP-LQPPS	Ahr_Human
.....	Consensus
LLYRARAKNSEYYVWLRTQAY AFL	Darnt
VMFRFRSKNQE-WLWMRTSSFT FQ	Harnt
NCYKFKIKDGS-FITLRSRWFS FM	Bmal1
SCYRLLSRNGR-FIYLNTKOFLEV	Met_Orf
IVFRLLTKNNRW TWVQS NARLLYK	Ahr_Human

Match Line to Fig. 6C

Match Line to Fig. 6H



Replacement Sheet

Match Line to Fig. 6A

370 N P Y T D E **V** E Y I V **C** T **N** S S G K
448 N P Y **S** D E I E Y I **C** T **N** T N V K N S S Q E P R P T L
425 N P W T K E **V** E Y I V S T **N** T V V
489 **D** R G S N K V H S F L C V N T L L . **D** E E A G R Q . . **K**
477 N . . . G R P D Y I I V T Q R P L T **D** E E G T E H L R **K**

463 A P T P Q Q Q Q Q Q Q R P G **S** A Q T **T** P V
558 R F S E I Y H N I N A **D** Q S K G I S S S T V P A T Q Q L
500 A E E I M E I H R I R G S S P **S** S C
673 **M** E S L M D D G Y S S P A N T L T L E E
477 S T A P F E N N F F N E S M N E C R **N** W Q D N T A P M G

636 T S P A R S **P** S G P **T** Y T Q
668 G V G S F Q T P **S** S F S **S** M S L P G A P T A **S** P G A A A
593 P S N D E A **A** M A V I M **S** L L E A D A G L G G P V D F S
870 **S** C I L S P A S S L S A S E A P D T P D P H S N T S P P
587 D S L S K S P F I P **S** D Y Q Q Q Q S L A L N **S** S C M V Q

621 A A D V G S H A D H V
700 L G D Q S N S Y N N E E F P D L T M F P P F S E
620
716
696 Y T Q N F I S C N Q P V L P Q H S K C T E L D Y P M G S

631
789
626
718
906 V K F

Consensus *Consensus #1*: When all match the residue of Met_Orf show the residue of Met_Orf. otherwise show **

Fig. 6E

Match Line to Fig. 6F



Replacement Sheet

Match Line to Fig. 6C

.....
Q Q Q E Q H V Y V Q A A P G V D - Y A R R E L T P V G S A
Q Q Q Q Q T E L D M V P G R D G L A S Y N H S Q V V Q P V
S P H S M D S M L P S G E G G P K R T H P T V P G I P G G
A P Q Q L E R I V L Y L I E N L Q K S V D S A E T V G G Q
L P L R T K N . . . G T S G K D S A T T S T L S K D S L N
.....

G T S P T P V A P N S
Q P S A S A G Q M L A Q I S R H S N P T Q G A T P T W T P
D I P S S G L L S G Q A Q E N P G Y P Y S D
K S V S V V N V T A A R K F Q Q E H Q K Q R E R D R E Q L
S K N S D L Y S I M K N L G I D F E D I R H M Q N E K F F
.....

P P P P P N A P G M W D W Q Q A G G H P H P P H P T A H P
G Q F Q T R T A E G V G V W P Q W Q G Q Q P H H R S S S S

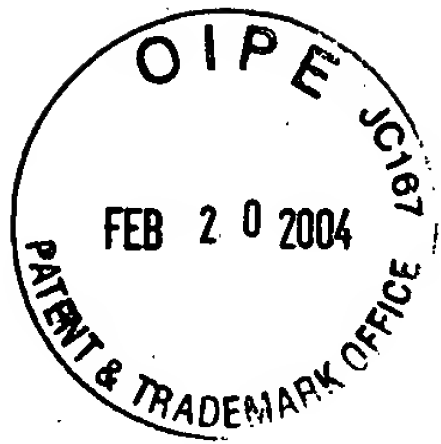
K H M Q V N G M F E N W N S N Q F V P F N C P Q Q D P Q Q
.....

N P Q S A I I T P Q T C Y A G A V S M Y Q C Q P E P Q H T
.....

Match Line to Fig. 6F

Match Line to Fig. 6H

Fig. 6G



Replacement Sheet

Match Line to Fig. 6D

.....	Consensus
T N D G M Y Q T H M L A M Q	Darnt
T T T G P E H S K P L E K S D G L F A Q D R D P	Harnt
T R A G A G K I G R M I	Bmal 1
G	Met_Orf
P S S L L A A M M Q Q D E S I Y L Y P A S S T S	Ahr_Human
.....	Consensus
W A A L R P Q Q Q Q Q Q P V T E G Y Q Y Q Q	Darnt
T T R S G F S A Q Q V A T Q A T A K T R T S Q F	Harnt
S S S I L G E N P H I G I D M I D N D Q G S S S	Bmal 1
K E R T N S T Q G V I R Q L S S C L S E A E T A	Met_Orf
R N D F S G E V D F R D I D L T D E I L T Y V Q	Ahr_Human
.....	Consensus
H H P H A H P G G P A G A G Q P Q G Q G V L R Y	Darnt
E Q H V Q Q P P A Q Q P G Q P E V F Q E M L S M	Harnt
.....	Bmal 1
.....	Met_Orf
Y N V F T D L H G I S Q E F P Y K S E M D S M P	Ahr_Human
.....	Consensus
.....	Darnt
.....	Harnt
.....	Bmal 1
.....	Met_Orf
H V G Q M Q Y N P V L P G Q Q A F L N K F Q N G	Ahr_Human
.....	Consensus
.....	Darnt
.....	Harnt
.....	Bmal 1
.....	Met_Orf
.....	Ahr_Human

Match Line to Fig. 6G

Fig. 6H



Replacement Sheet

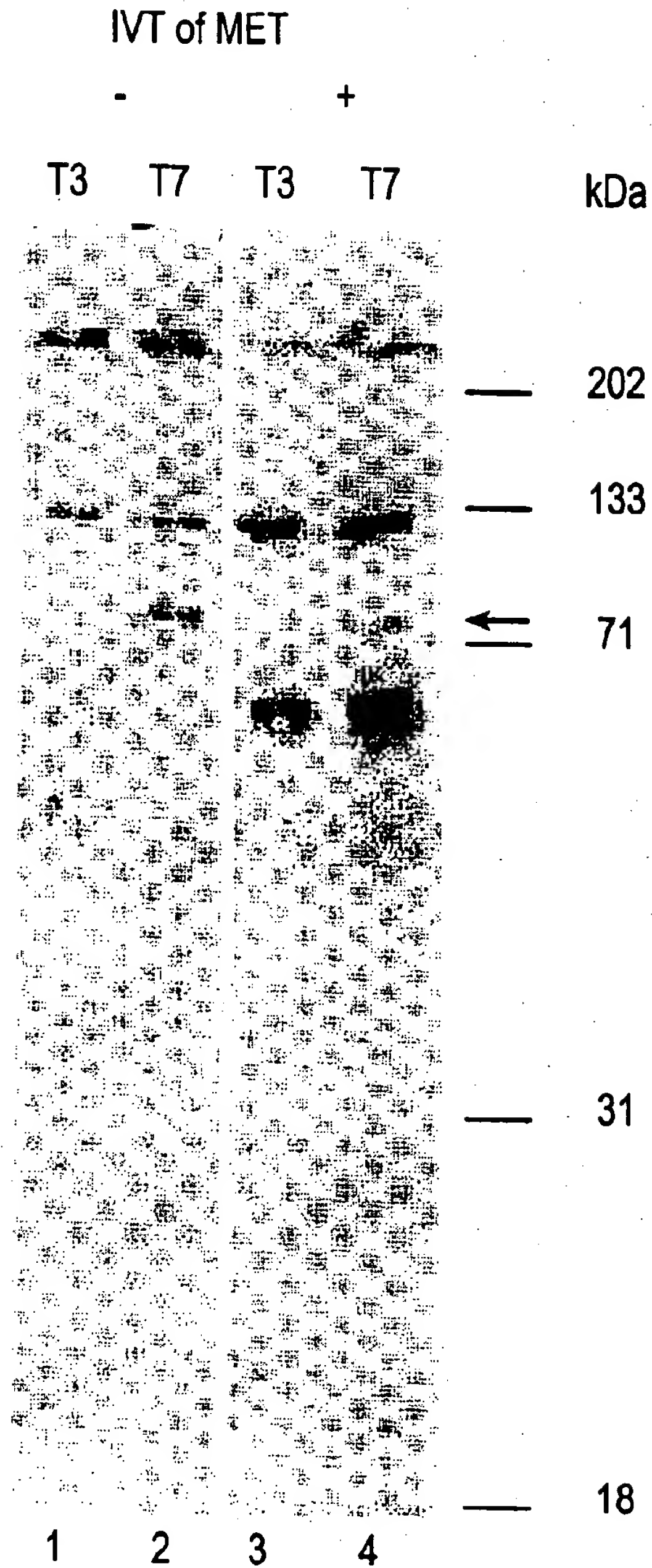


Fig. 1



Replacement Sheet

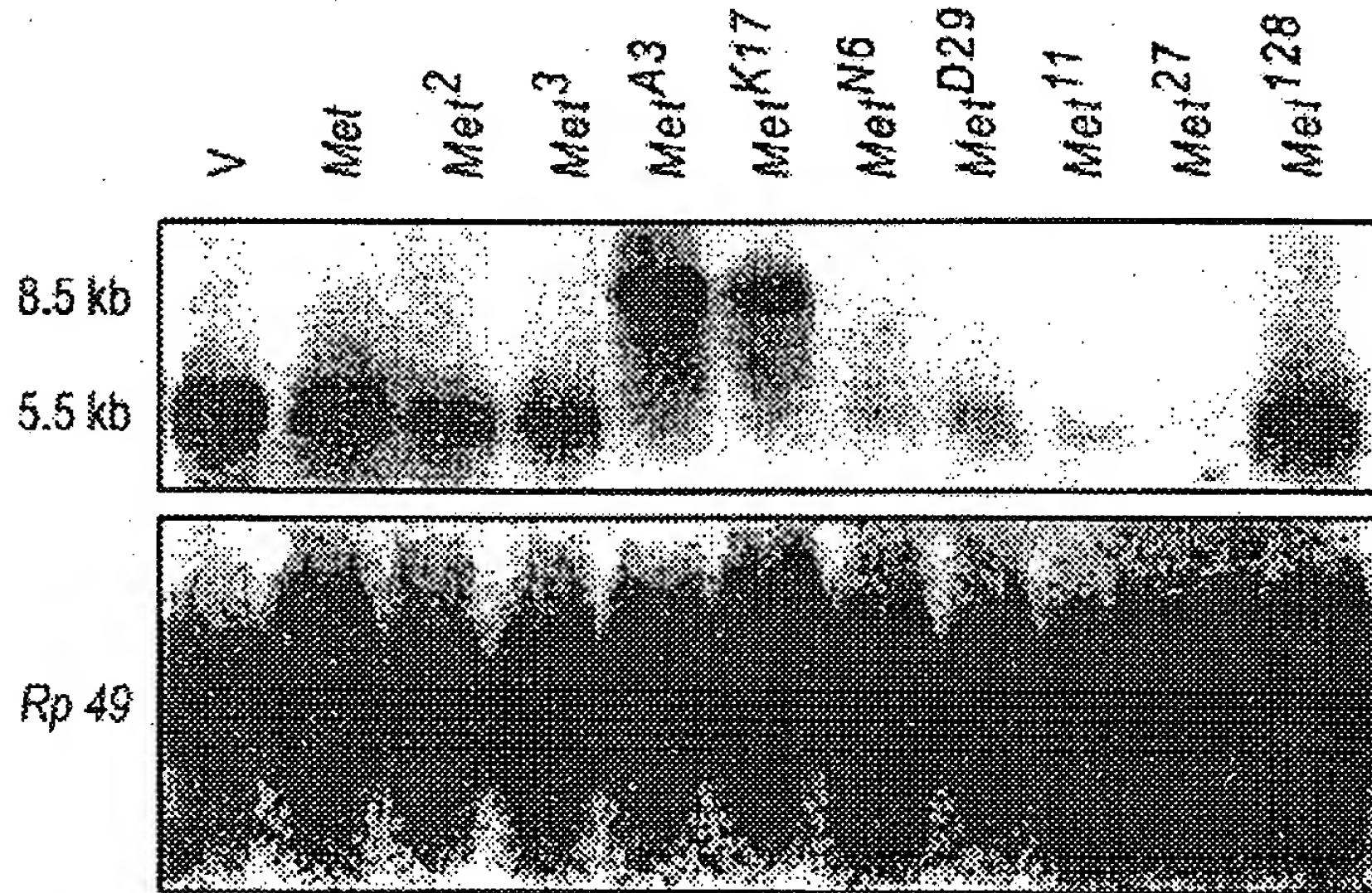


Fig. 8

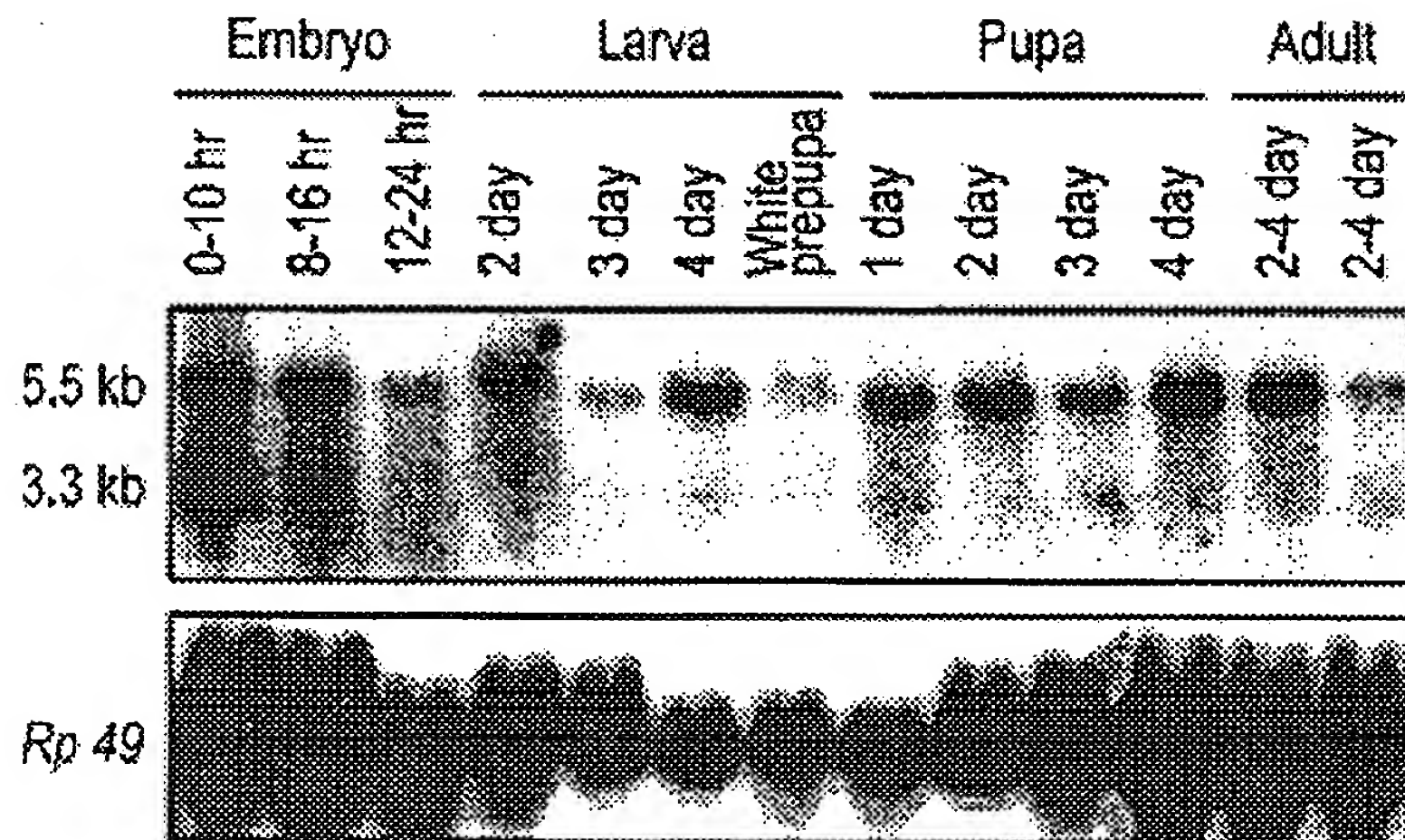


Fig. 9